us-09-625-573-2.rsp

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

May 19, 2003, 16:36:02; Search time 15.7956 Seconds (without alignments) 982.052 Million cell updates/sec Run on:

US-09-625-573-2 1970 1 MLSTSRSRFIRNTNESGEEV.....GKGKSIGRAPEASLQDKEGA 374 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 hotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					SUMMARIES	
Result		% Ouerv				
No.	Score	Match	Length	DB	QI	Description
ä	1970		374	Н	CKR2_HUMAN	597 homo sa
7	1614.5		360	Н	CKR2_MACMU	3 тасаса
3	1346.5			Н	CKR2_RAT	ratt
4	1332.5	67		Н	CKR2_MOUSE	P51683 mus musculu
5	1244	63	354	Η,	CKR5_MOUSE	
9	1236	62	352	٦	CKR5_CERTO	
7	1236		352	Н	CKR5_HYLLE	
80	1230		352	Н	CKR5_MACMU	
6	1230		352	7	CKR5_PANTR	P56440 pan troglod
10	1230		352	Н	CKR5_PONPY	097881 pongo pygma
11	1230		354	Н	CKR5_RAT	
12	1228		352	٦	CKR5_GORGO	
13	1228		352	Н	CKR5_PAPHA	
14	1224	62.	352	٦	CKR5_HUMAN	
15	1224	62.	352	7	CKR5_PYGNE	
16	1223	62.		Н	CKR5_PYGBI	
17	1223	62.		Н	CKR5_TRAFR	
18	1223	62.		Н	CKR5_TRAPH	
19	1211	61.		٦	CKR5_CERAE	
20	967.5	49.		Η,	CKR1_HUMAN	
21	951.5	48.3	359	Н	CKR3_MOUSE	
22	945	48.		Н	CKR3_RAT	
23	931.5	47.		Н	CKR3_CAVPO	
24	911.5	46.		1	CKR1_MACMU	maca
25	899.5	45.		Н	CKR1_MOUSE	mus m
26	886.5	45.		-	CKR3_HUMAN	
27	876	44		Н	CKR3_MACMU	
. 28	867	44.		Н	CKR3_CERAE	cerc
29	833	42.		7	CKR4_MOUSE	mus m
30	831.5	4		-	CKR4_HUMAN	Ollion (
31	731	37.		Н	CKRV_MOUSE	mus m
32	723	36.7		Н	CKR8_HUMAN	homo sa
33	716.5	m	356	Н	CKR8_MACMU	097665 macaca mula

484 mus musculu	P35411 rattus norv	1238 homo sapien	:0d9 mus musculu	590 homo sapien	248 homo sapien	3707 mus musculu	774 mus musculu	3027 rattus norv	1686 homo sapien	1689 mus musculu	9wut7 mus musculu
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CKR8_MOUSE	C3X1_RAT	C3X1_HUMAN	C3X1_MOUSE	CKD6_HUMAN	CKR7_HUMAN	CKD6_MOUSE	CKR7_MOUSE	CKD6_RAT	CKR9_HUMAN	CKR6_MOUSE	CKR9_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLFHIALGCRIAPLQRPVCGGPGVRPGKNVKVTTQGLLDGR
GKGKSIGRAPEASLQDKEGA -> RYLSVFFRKHITKRFCK
            FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.

Transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.

SUBCELLULAR LOCATION: Integral membrane protein.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 MLVVLILINCKKIKCITDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
                                                                                                                SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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; Pred. No. 3.7e-115;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
 Immunol. 165:5295-5303(2000)
                                                                                                                                                                                                                                                                                AAA19120.1; -.
BAA06253.1; -.
AAC51637.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 AA; 41914 MW;
                                                                                                                                                                                                                                                                                          EMBL, D29904, BAA06253.1;
EMBL, U80924, AAC51637.1;
EMBL, U80924, AAC51636.1;
EMBL, U95628, AAS57791.1;
EMBL, U95626, AAS57791.1;
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                                                                                                     PTM: N-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                        HGNC:1603; CCR2.
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               181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                                                              241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                                                                                                                              301 NPIIYAFVGEKFRSLFHIALGCRIAPLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
                                                                                                                                                     receptors.";
AIDS Res. Hum. Retroviruses 17:981-986(2001).
-!- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.
TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 2 (C-C CRR-2) (CC-CKR-2) (CCR-2) (CCR2)
(CNDOCCYTE chemoattractant protein 1 receptor) (MCP-1-R) (CCR2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_Protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Alternative splicing.
                                                                               MEDLINE=21354176; PubMed=11461684;
Margulies B.J., Hauer D.A., Clements J.E.;
"Identification and comparison of eleven rhesus macague chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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INTERPRO, IPR000277; GPCR_Rhodpsn.
PFam, PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
                                                                                                                                                                                                                   361 GRAPEASLODKEGA 374
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80
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1114
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1153
206
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018793;
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-i- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
CHEMOKINES. TRANSDOCES A SIGNAL BY INCREASING THE INTRACELLULAR
CALCIUM IONS LEVEL (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98318173; PubMed-9655467; Jaing Y., Feng L., Sonntag M.K., Jaing Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., deFiebre C.M., Pennell N.A., Streat W.J., Harrison J.K.; "Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                            61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPIMAHSAANEWVFGNAMCKLFTGLY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                          MLSTSRSRFIRNTNESGEEVITFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
                                                                                                                                                                                                                           OCT-2001 (Rel. 40, Last sequence update)
OCT-2001 (Rel. 40, Last annotation update)
chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                      HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK
                                                                                                                                                                                                                                                                                                                                                                               CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR
                                                                                  (POTENTIAL)
                                                                                                                                                                                3;
                                                                                                                                                    DB 1; Length 360;
                                                                                                                                                                                 4; Indels
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                             N-LINKED (GLCNAC. . .) (PC SULFATION (BY SIMILARITY).
BY SIMILARITY.
4B2552BCE913FE9F CRC64;
                                                    7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                     Score 1614.5; DB Pred, No. 3.1e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 AA
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergic encephalomyelitis.";
                                                                                                                           41139 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 NPIIYAFVGEKFRRYLSMF 319
                                                                                                                                                     82.0%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPIIYAFVGEKFR---SLF 316
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
2226
2243
2268
2268
309
360
14
26
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Sprague-Dawley;
                                                                                                                          360 AA;
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MACROPHAGES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR CMKBR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                                                                 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKR2_RAT
055193;
              DOMAIN
TRANSMEM
                                                                                  CARBOHYD
                                                                                                                                                    Query Match
                                                      TRANSMEM
                                                                                                              DISULFID
                                                                                                                           SEQUENCE
  TRANSMEM
                                                                                                  MOD_RES
                                                                                                                                                                       Local
                                          DOMAIN
                                                                      DOMAIN
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Matches
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 MLVIIILISCKKLKSMTDIYLFNLAISDLLFLLTLFFWAHYAANEWVFGNIMCKLFTGLY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 ILSTSHSLFPRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 2 (C-C CKR-2) (CC-CKR-2) (CCR-2)
(JE/FIC receptor) (MCP-1 receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.4%; Score 1346.5; DB 1; Length 373; 76.9%; Pred. No. 1.1e-76; ive 25; Mismatches 45; Indels 7;
                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
2E7BB012F5D6FD09 CRC64;
                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 NPIIYAFVGEKFRYLSIFFRKHIAKNLCKQCPV 347
                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_COUPLED receptor; Transmembrane.
DOMAIN
                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                 InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42763 MW;
                                                                                                                    EMBL; U77349; AAC03242.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 76.9
Matches 257; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                301
322
373
203
                                                                                                                                                   PF00001; 7tm_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKR2_MOUSE | P51683; Q61172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCR2 OR CMKBR2
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                                                                                                                                            chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=97026720; PubMed=8872898;

MEDLINE=97026720; PubMed=8872898;

Meesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,

Post T.W., Gerard C., Dorf M.E.;

"Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";

KC or new MCP-1 receptor.";

J. Neurosci. Res. 45:382-391(1996).

-I- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5
                                                                                                                             Molecular cloning and functional expression of murine JE (monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,
BUT NOT IN NONHEMATOPOIETIC CELL LINES.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
dammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                   Kurihara T., Bravo R.;
"Cloning and functional expression of mCCR2, a murine receptor for
                                                    SEQUENCE FROM N.A.
MEDLINE=96205938; Pubmed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR, (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
5 (POTENTIAL).
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6 (POTENTIAL).
7 (POTENTIAL).
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8 YIRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                      the C-C chemokines JE and FIC.";
J. Biol. Chem. 271:11603-11606(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:106185; Cmkbr2.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                               MEDLINE=96216064; PubMed=8662823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U47035; AAC52453.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U51717; AAC52557.1; -. EMBL; U56819; AAC52784.1; -.
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                STRAIN=BALB/C;
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61 MLVVLILINCKKLKCLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLY 120
                                                                                                                                                                                                                                                                                                                                                                                           181 CQKEDSVYVCGPYFPRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 HIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 AVRVIFTIMIVYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemoattractant protein 1) and murine macrophage inflammatory protein lalpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9 ":
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                            1 MLSTSRSRFIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGN 60
                                                                                                                                                                                                                                                                                     14 ILSTSHSLFTRSIQELDEGATTPYDYDDGEPCHKTSVKQIGAWILPPLYSLVFIFGFVGN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CKR5_MOUSE STANDARD; PRT; 354 AA.
P51682; Q61867; P97405; O35313; P97308; O35891;
01-0CT-1996 (Rel. 34, Created update)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and functional expression of murine JE (monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6, and NIH Swiss; TISSUE-Liver, Kidney, and Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L., Charo I.F.;
                                                                                                                                                                  7;
                                                                                                  DB 1; Length 373;
                                                                                                                                                                  46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
   V -> G (IN REF. 1).
FA012C10F4C9325A CRC64;
                                                                                           ; Score 1332.5; DE; Pred. No. 8e-76; 26; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammatory protein-1 alpha receptor.";
J. Biol. Chem. 271:14445-14451(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
MEDLINE-96278910; PubMed=8662890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors on chromosome 9.";
J. Biol. Chem. 271:7551-7558(1996).
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MEDLINE=96205938; Pubmed=8631787;
264 264 V
373 AA; 42782 MW;
                                                                                                  67.68;
                                                                                                                                76.3%;
                                                                                                                                                               Matches 255; Conservative
                                                                                           Query Match
Best Local Similarity
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                              SEQUENCE
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; /tm_l; 1.
PRINTS; PR00237; GCRRHDODPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.
32 EXTRACELLULAR (POTENTIAL).
                                                                           MEDILINE=97404635; PubMed=9261347;
Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.,
"Two distinct CCR5 domains can mediate coreceptor usage by human
immunodeficiency virus type 1.";
J. Virol. 71:6305-6314(1997).
                                                                                                                                                                       TO MIP-1-ALPHA,
                                                                                                                                                     Kuhmann S.E., Platt E.J., Kozak S.L., Kabat D:;
Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
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7 (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
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MEDLINE=98001387; PubMed=9343222;
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EMBL: U68565; AAB37273.1; -.
EMBL: U83327; AAC53386.1; -.
EMBL: AF022990; AAC53389.1; -.
EMBL: AF019772; AAB71183.1; -.
                                                                                                                                                                                                                                                                                                                                                                            D83648; BAA12024.1; -.
                                            Virol. 71:8642-8656(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 VYFLEWTPYNIVLLTTTEQEFFGLNNCSSSNRLDQAMQATETLGMTHCCLNPVIYAFVGE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                          75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYTDIYLLNLAISDLLFLTLPFWAHYAANEWIFGNIMCKVFTGVYHIGYFGGIFFIILL 124
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                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                17 GEEVTTFFDYDYG--APCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLK 74
                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
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P -> L.

I -> V.

V -> A.

V -> A.

IIIN REF. 2).

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                                                                                                                                                                                                                                                                               Pred. No. 2.2e-70
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                     29; Mismatches
                                                                                                                                                                                                                                                         63.1%; Score 1244; 75.3%; Pred. No. 2.
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MEDLINE=98321155; PubMed=9656999;
                                                                                                                                                                                                              40863 MW;
                                                                                                                                                                                                                                                                                                       Conservative
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145
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                  EMBL; AF051902; AAC39830.1; -
EMBL; AF051904; AAC39831.1; -
EMBL; AF051904; AAC39831.1; -
EMBL; AF051905; AAC39833.1; -
EMBL; AF051905; AAC39833.1; -
EMBL; PR000207; GPCR_Rhodpsn.
PRINTS; PR00021; GPCR_RHODPSN.
PROSITE; PS00237; GPCR_RHODPSN.
PROSITE; PS0262; G_PROTEIN_RECEP_FI_2; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_FI_2; 1.
G_PROTEIN; Transmembrane; Glycoprotein; Sulfation.

EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Y -> D (IN ISOLATE 087).
V -> G (IN ISOLATE 087).
M -> K (IN ISOLATE 087).
L -> V (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
V -> G (IN ISOLATE 089).
V -> C (IN ISOLATE 089).
Y -> L (IN ISOLATE 079).
Y -> L (IN ISOLATE 079).
T -> I (IN ISOLATE 079).
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SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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ilarity 77.3%; Pred. No. 6.9e-70;
Conservative 26; Mismatches 32
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26; Mismatches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL.outstation the European Bioinformatics Institute. There are no restfictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                       SQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=99416438; PubMed=10486970;

Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

"Sequence evolution of the CCR5 chemokine receptor gene in primates.";

"Sequence evolution of CCR5 chemokine receptor gene in primates.";

MOL Biol. Evol. 16:1146.1154(1999).

-I. FUNCTION: RECEPTOR FOR A CC TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE

INTRE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR

"THE GRANULOCYTIC LINEAGE PROLIFERATION OR THE GRANULOCYTIC LINEAGE PROLIFERATION 
                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUM-2002 (Rel. 41, Last annotation update)
C-C chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSTIE; PS00237; G_PROTEIN_RECEP_FI_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
DOMAIN 1 30 EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                   Hylobates leucogenys (White-cheeked gibbon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hylobatidae, Hylobates.
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thes 34; Indels
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CTTOPLASHIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASHIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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                             352 AA
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25; Mismatches
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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352 AA;
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CKR5_HYLLE
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133 AVFALKARIVTEGVVISVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 IVLLLNTFOEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIXAFVGEKFRNYLLVFF 312
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
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MEDLINE=97213934; PubMed=9060623;
Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
"Genetically divergent strains of simian immunodeficiency virus use CCR5 as a coreceptor for entry.";
J. Virol. 71:2705-2714(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and Macaca nemestrina (Pig-tailed macaque).
Eukaryota: Metazoa; Chorodata: Craniata: Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=M...unlatta, M.fascicularis, and M.nemestrina; MEDLINE=97268687; PubMed=9108095; Badinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; Differential utilization of CCRS by macrophage and T cell tropic simian immunodeficiency virus strains."; Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
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85 AISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVH
                                                                                                                                  145 AVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RGWNN
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MEDLINE=97184592;
Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu J.
Newman W., Gerard N., Gerard C., Sodroski J.;
"Utilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
SIVMac239.";
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MEDLINE=21354176; PubMed=11461684;
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Macaca mulatta (Rhesus macaque),
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NCBI_TaxID=9544, 9541, 9545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQREGLHYTCSSHFPYSQYQF 189
FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIIGLTIDRYLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
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                                                                                                                                                                                                                                                                                                                                           PFam; PF00001; / cur_1, ...
PRINTS; PR00237; GPCRHDOPSN.
PROSTTE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSTTE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
30 EXTRACELLUIAR (POTENTIAL).
                                                                        SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
N-LINKED (GLOAAC...) (POTENTIAL).
M -> I (IN REF. 3).
I -> M (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33; Indels 12;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                           Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40507 MW;
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                                                               DIFFERENTIATION.
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241
292
352 AA;
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CONFLICT
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                MEDLINE-98022612; Pubmed-9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
Ho D.D.;
                                                                                                                                                                        CKR5_PANTR STANDARD; PRT; 352 AA.
P56440; 002778;
115-JUL-1998 (Rel. 36, Created)
115-JUL-1998 (Rel. 36, Last sequence update)
116-OCT-2001 (Rel. 40, Last annotation update)
C-C_chemokine_receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lacharova V., Zachar V., Goustin A.S.;
"Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97268687; PubMed-9108095;
Eduger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
"Differential utilization of CRS by macrophage and T cell tropic simian immunodeficiency virus strains.";
Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
                                                                                                                                                                                                                                                                        CCRS OR CMKBRS.
Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Zimmerman P.A., Buckler-White A., Alkhatib G.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                317 -----HIA 319
                                                                                              310 VFFQKHIA 317
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9598;
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EMBL; AF005663; AAB62557.1; -. EMBL; U94329; AAB58446.1; -.

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82 LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 YDIDYYTSEPCQKINVKQIAARLEPLYSLVFIFGFVGNMLVILLLINCKRLKSMTDIYL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
                            EMBL; 099797; AAC03717.1; -
Interpro. IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1: 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00227; G_PROTEIN_RECEP_F1_1; 1.
G_PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_PROTEIN_STATEMENTANE.
TRANSMEM 31 58 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> S (IN REF. 1).
4A33E698B80FE34C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 352;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
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EMBL; AF011542; AAB65742.1; -.
EMBL; U97666; AAC51670.1; -.
EMBL; AF011540; AAB65740.1; -.
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Watches 237; Conserv
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TRANSMEM
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CARBOHYD
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258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
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                                                                                                                                                                                                                                                                                                             STRAIN=Wistar; TISSUE=Brain;
                                                                                                                                         STANDARD;
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91
104
1126
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                                                        317 -----HIA 319
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                                                                               310 VFFOKHIA 317
                                                                                                                                                                                                                alpha receptor).
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71
92
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O08556;
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CKR5_RAT
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Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";
Mol. Biol. Evol. 16:1145-1154(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 IVHAVFALKARTVTFGVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSHFPYSQYQF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
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                                                                                                     -i- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA
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                                                                                                               MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDOCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                      G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation. DOMAIN 130 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                              SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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; Pred. No. 1.6e-69;
25; Mismatches 34; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
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SULFATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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Pfam; PF00001; 7tm_1; 1.
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Matches 237; Conservative
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260
277
301
352
178
                                                                                                                                                         DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 AA;
                                                 SEQUENCE FROM N.A.
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90
103
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                          NCBI_TaxID=9600;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley;
MEDLINE=98318173; PubMed=9655467;
Jiang Y., Salafranca M.N., Adhlkari S., Xia Y., Feng L., Sonntag M.K.,
Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
"Chemokine receptor expression in cultured glia and rat experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergic encephalomyelitis.";
J. Neuroimmunol. 86:1-12(1998).
-:- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
250 PYNIVLLINTEQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPITAFVGEKFRNYLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
03-0MXY-2000 (Rel. 39, Last annotation update)
C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (MIP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and uprequiation of its mRNA in ischemic and endotoxinemic rat brain."; J. Neurosci. Res. 53:16-28(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98334064; PubMed-9670989;
Spleiss O., Gourmala N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00001; /tmm.t, repropersors Prints; PR00237; GPRRHODDSN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE: PS050262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
32 EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                        65 SMTDIYLFNLAISDLLFLTLFFWAHYAANEWVFGNIMCKLFTGIYHIGYFGGIFFIILL 124
                                                                                                                                                                                                                                                       135 TIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYF 194
                                                                                                                                                                                                                                                                    195 ----PRGWNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMI 250
                                                                                                                                                                                                                                                                                                                                                   251 VYFLFWTPYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGE 310
                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C_chemokine_receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                  Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Gorilla.
                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL). 77EDB368AA4C868D CRC64;
                                                                                                                    Score 1230; DB 1; Length 354;
                                                                                                                            75.0%; Pred. No. 1.06-09;
live 29; Mismatches 42; Indels
                        6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
  5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                              41030 MW;
                                                                                                                   62.4%;
                                                                                                                                           Conservative
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237
262
279
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303
180
270
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270
354 AA;
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                                                                                                                              Similarity
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                                                                                                                                       Matches 231;
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P56439;
            DOMAIN
TRANSMEM
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DISULFID
                                              TRANSMEM
 TRANSMEM
                                                                                CARBOHYD
                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
                                                                          Pfam; PF00001; /Lm_1, 1.

PRINTS; PR00237; GPRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 FDYDY -- GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-C chemokine receptor type 5 (C-C CRR-5) (CCR-5) (CCR5).
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 352;
                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
SULFATION (BY SIMILARITY).
W. DOEGFCB9FE5EAC84 CRC64;
                                                                                                                                               1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
SXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
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6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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5 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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25; Mismatches
                                                                                                                                                                                                                                    4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%; Score 1228; 76.9%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Papio hamadryas (Hamadryas baboon), and Papio anubis (Olive baboon).
                                                EMBL; AF005659; AAB62553.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     40515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     237; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     352 AA;
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Homo sapiens (Human)
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                                                               Best Local Similarity
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MOD_RES
MOD_RES
CARBOHYD
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                                                     Query Match
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                                                                                                                                                                                                                                                                     Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
                                                                                                                                                                          SPECIES-P. hamadryas;
MEDLINE-99210133; PubMed=10195758;
Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
"Species-specific changes in the CCR5 gene from African and Asian nonhuman primates.";
                                                                                                                                                                                                                                                                                                                  INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                    Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.; "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.", Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                               AIDS Res. Hum. Retroviruses 15:479-483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL)
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                                                                   SPECIES-P.hamadryas;
MEDLINE-97268687; PubMed-9108095;
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68
89
102
1124
1141
1166
1198
2318
2335
                         Cercopithecinae; Papio.
NCBL_TaxID=9557, 9555;
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352
178
                                                                                                                                                                                                                                                                                                                                          DIFFERENTIATION
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             SPECIES=P. anubis;
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59
69
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103
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142
167
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MEDLINE=96291862; PubMed=8663314; Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.; Molecular cloning and functional characterization of a novel human CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."; J. Blol. Chem. 271:17161-17166(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 IVHAVFALKARTVTFGVVTSVITWVAVFASLPGIIFTRSQREGLHYTCSSHFPYSQYQF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 PYNIVLLINTEQEFFGLNNCSSSNRLDQAMQVTETLGMTHCINFITAFVGEKFRNYLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
                                                                                                                                                                                                                                                                                                                                                                                          82 ENLAISDELFLITEPEWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                      24 FDYDY -- GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
                                                                                                                                                                                                                                                                                                         10 YDIDYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNILVVLILINCKRLKSWTDIYL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         014708; 015538; Q9UPA4; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) (CC chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCRF) (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-96295970; Pubmed-8699119; Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.; "Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKRS_HUMAN STANDARD; PRT; 352 AA.
PS1661; 014692; 014693; 014695; 014696; 014699; 014700; 014701; 014702; 014703; 014704; 014705; 014707;
                                                          (POTENTIAL).
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                                                                                                                                                 Length 352;
                                                                                                                                                                                                                  Indels
SULFATION (BY SIMILARITY). SULFATION (BY SIMILARITY).
                                                                   SE1504A9BA1FE8B2 CRC64;
                                                                                                                                                                                                                  33;
                                                                                                                                                 Score 1228; DB 1;
Pred. No. 2.1e-69;
                                                             (GLCNAC
                                                                                                                                                                                                                  26; Mismatches
                                                          N-LINKED
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Biochemistry 35:3362-3367(1996).
                                                                                          40489 MW;
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SULFATION
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SEQUENCE FROM N.A., AND POLYMORPHISMS.
MEDLINE-98022612; Pubmed-9359654;
Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98001387; PubMed=9343222; MEDLINE=98001387; PubMed=9343222; Muhamann S.E., Platt E.J., Kozak S.L., Kabat D.; Kozuk S.L., Kapat D.; Mupurphisms in the CCR5 genes of African green monkeys and mice implicate specific amino acids in infections by simian and human immunodeficiency viruses."; J. Virol. 71:8642-8656(1997).
SEQUENCE FROM N.A.

MCCOmbie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E.,
Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
Submitted (MAY-1997) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."; AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
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MEDLINE-98049523; PubMed=9388201; Mummidi S., Ahuja S.K.; Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.; Mummidi S. chemokine receptor 5 (CCR5) gene. Multiple transcripts with 5'-end heterogeneity, dual promoter usage, and evidence for polymorphisms within the regulatory regions and noncoding exons."; J. Biol. Chem. 272:30662-30671(1997). SEQUENCE FROM N.A., AND VARIANT ARG-178. Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,

Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases. Debre P.;

CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
MEDLINE-96560017; PubMed-8649511;
Deng H., Liu R., Ellmeler W., Choe S., Unutmaz D., Burkhart M.,
di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
"Identification of a major co-receptor for primary isolates of

Nature 381:661-666(1996).

entry into CD4+ cells is mediated by the chemokine receptor Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y., Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P., CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION. MEDLINE=96260018; PubMed=8649512; Paxton W.A.; CC-CKR-5

Nature 381:667-673(1996).

MEDLINE=99189752; PubMed=10089882;

Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M., Gerard N.P., Gerard C., Sodroski J., Choe H.; "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation; Polymorphism.

1 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL). EXTRACELLULAR (POTENTIAL). EXTRACELLULAR (POTENTIAL).

30 58 68 102 124 141

31 59 69 90 103 125

FRANSMEM PRANSMEM **FRANSMEM TRANSMEM**

DOMAIN DOMAIN DOMAIN DOMAIN

3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).

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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. InterPro; IPR000276; GPCR_Rhodpsn. EMBL, AF011500, AAB65701, EMBL, AF011501, AAB65701, EMBL, AF011501, AAB65701, EMBL, AF011502, AAB65701, EMBL, AF011503, AAB65702, EMBL, AF011505, AAB65702, EMBL, AF011505, AAB65706, EMBL, AF011509, AAB65709, EMBL, AF011510, AAB65709, EMBL, AF011510, AAB65711, EMBL, AF011511, AAB65712, EMBL, AF011513, AAB65712, EMBL, AF011513, AAB65712, EMBL, AF011513, AAB65712, EMBL, AF011514, AAB65712, EMBL, AF011514, AAB65712, EMBL, AF011521, AAB65721, EMBL, AF011521, AAB65722, EMBL, AF011523, AAB65722, EMBL, AF011523, AAB65722, EMBL, AF011524, AAB65722, EMBL, AF011524, AAB65722, EMBL, AF011529, AAB65722, EMBL, AF011529, AAB65720, EMBL, AF011520, AA EMBL; U57494; AAC50598.1; --EMBL; U57840; AAB17071.1; --EMBL; U9526; AAB57793.1; --EMBL; U83326; AAC51797.1; --EMBL; X91492; CAA62796.1; -. EMBL; AF011532; AAB65732.1; EMBL; AF011533; AAB65733.1; EMBL; AF011534; AAB65734.1; EMBL; AF011535; AAB65735.1; EMBL; AF011536; AAB65736.1; AF011531; AAB65731.1; AAD18131.1; AF031237; AAB94735 EMBL; AF011537; AAB65737 Pfam; PF00001; 7tm_1; 1 HGNC:1606; CCR5. GLYCOSYLATION EMBL; AF031237; EMBL; AF052539; 601373; Genew; EMBL; THE HELE THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE THE TENT OF THE THE TENT OF T Ļì.

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MEDLINE=99416438; PubMed=10486970;

MEDLINE=99416438; PubMed=10486970;

Saguence evolution of the CCR5 chemokine receptor gene in primates.";

Mol. Biol. Evol. 16:1145-1154(1999).

-1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,

MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY

INVERASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE

IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 PYNIVLLINTEQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPLIYAFVGEKFRNYLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pygathrix nemaeus (Dove langur).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                               258 PYNIVILLNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRSLF- 316
                                                                                                                                                                                                                                                                                                                                          198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT 257
                                                                                                                                                                                                                                                                                                                             LNLAISDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLA 141
                                                                                                                                                                                                                                                                                                                                                                               IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCQKEDSVYVCGPYFP----RG 197
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                           FDYDY --GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVLILINCKKLKCLTDIYL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
C-C chemokine_receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR5).
                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                           Score 1224; DB 1; Length 352; Pred. No. 3.8e-69;
                                                                                                                                                                                                                                                   34; Indels
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EXTRACELLULAR (POTENTIAL)
                                     6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                       CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
             5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                  Y -> D (IN INCCR5-71A).
/FTId=VAR_003481.
                                                                                                                                                                                      /FTId=vAR_011839.
R -> H (IN INCCR5-72A).
                                                               (POTENTIAL).
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                                                                                                             SULFATION.
SULFATION.
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76.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 VFFQKHIA 317
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14
15
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199
219
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236
261
278
302
101
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097882;
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nes 235;
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PROSITE; PS50262; G_PROTEIN_RECEP_FI_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

CAPACITY (POTENTIAL)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 WNNFHTIMRNILGLVLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 352;
                                                                                                                                                                                                                                        TO POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).
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ULFATION (BY SIMILARITY)
ULFATION (BY SIMILARITY)
FE4F9D98D3B3E861 CRC64;
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SULFATION (BY SIMILARITY)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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